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☐ 1: S66100. conserved hypothe...[gi:2127048]

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LOCUS S66100 233 aa linear BCT 18-AUG-2000
DEFINITION conserved hypothetical protein yacB - Bacillus subtilis.
ACCESSION S66100
VERSION S66100 GI:2127048
DBSOURCE pir: locus S66100;

summary: #length 233 #molecular-weight 26217 #checksum 5610
;
genetic: #gene yacB #start_codon TTG
;
superfamily: Streptomyces coelicolor hypothetical protein SCE94.31c
;
PIR dates: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change
18-Aug-2000

KEYWORDS

SOURCE

Bacillus subtilis

ORGANISM

Bacillus subtilis

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

REFERENCE

1 (residues 1 to 233)

AUTHORS

Ogasawara,N., Nakai,S. and Yoshikawa,H.

TITLE

Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chromosome containing the replication origin

JOURNAL

DNA Res. 1 (1), 1-14 (1994)

MEDLINE

96051385

PUBMED

7584024

REFERENCE

2 (residues 1 to 233)

AUTHORS

Kunst,F., Ogasawara,N., Moszer,I., Albertini,A.M., Alloni,G., Azevedo,V., Bertero,M.G., Bessieres,P., Bolotin,A., Borchert,S., Boriss,R., Boursier,L., Brans,A., Braun,M., Brignell,S.C., Bron,S., Brouillet,S., Bruschi,C.V., Caldwell,B., Capuano,V., Carter,N.M., Choi,S.K., Codani,J.J., Connerton,I.F., Cummings,N.J., Daniel,R.A., Denizot,F., Devine,K.M., Duesterhoeft,A., Ehrlich,S.D., Emmerson,P.T., Entian,K.D., Errington,J., Fabret,C., Ferrari,E., Foulger,D., Fritz,C., Fujita,M., Fujita,Y., Fuma,S., Galizzi,A., Galleron,N., Ghim,S.Y., Glaser,P., Goffeau,A., Golightly,E.J., Grandi,G., Guiseppi,G., Guy,B.J., Haga,K., Haiech,J., Harwood,C.R., Henaut,A., Hilbert,H., Holsappel,S., Hosono,S., Hullo,M.F., Itaya,M., Jones,L., Joris,B., Karamata,D., Kasahara,Y., Klaerr-Blanchard,M., Klein,C., Kobayashi,Y., Koetter,P., Koningstein,G., Krogh,S., Kumano,M., Kurita,K., Lapidus,A., Lardinois,S., Lauber,J., Lazarevic,V., Lee,S.M., Levine,A., Liu,H., Masuda,S., Maueel,C., Medigue,C., Medina,N., Mellado,R.P., Mizuno,M., Moestl,D., Nakai,S., Noback,M., Noone,D., O'Reilly,M., Ogawa,K., Ogiwara,A., Oudega,B., Park,S.H., Parro,V., Pohl,T.M., Portetelle,D., Porwollik,S., Prescott,A.M., Presecan,E., Pujic,P., Purnelle,B., Rapoport,G., Rey,M., Reynolds,S., Rieger,M., Rivolta,C., Rocha,E., Roche,B., Rose,M., Sadaie,Y., Sato,T., Scanlon,E., Schleich,S., Schroeter,R., Scoffone,F., Sekiguchi,J., Sekowska,A., Seror,S.J., Serror,P., Shin,B.S., Soldo,B.,

Sorokin,A., Tacconi,E., Takagi,T., Takahashi,H., Takemaru,K.,
Takeuchi,M., Tamakoshi,A., Tanaka,T., Terpstra,P., Tognoni,A.,
Tosato,V., Uchiyama,S., Vandenbol,M., Vannier,F., Vassarotti,A.,
Viari,A., Wambutt,R., Wedler,E., Wedler,H., Weitzenegger,T.,
Winters,P., Wipat,A., Yamamoto,H., Yamane,K., Yasumoto,K., Yata,K.,
Yoshida,K., Yoshikawa,H.F., Zumstein,E., Yoshikawa,H. and
Danchin,A.

TITLE The complete genome sequence of the gram-positive bacterium
Bacillus subtilis

JOURNAL Nature 390 (6657), 249-256 (1997)

MEDLINE 98044033

PUBMED 9384377

FEATURES Location/Qualifiers

source 1..233

/organism="Bacillus subtilis"

/db_xref="taxon:1423"

Protein 1..233

/product="conserved hypothetical protein yacB"

ORIGIN

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61 iissvvpim falermctky fhiepqivgp gmktglniky dnpkevgadr ivnavaaahl
121 ygnplivvdf gtattcyid enkqymggai apgitistea lysraaklpr ieitrpdnii
181 gkntvsamqs gilfgyvqv egivkrmkwq akqdprrlq eawrrslrtn qiv

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